OIPE

RAW SEQUENCE LISTING   DATE: 12/19/2001
PATENT APPLICATION: US/09/767,597   TIME: 13:23:59

Input Set : **N:\Crf3\RULE60\09767597.txt**
Output Set: **N:\CRF3\12192001\I767597.raw**

```
 3 <110> APPLICANT: Jegla, Timothy James
 4        ICAgen, Inc.
 6 <120> TITLE OF INVENTION: Human HAC3
 8 <130> FILE REFERENCE: 018512-002210US
10 <140> CURRENT APPLICATION NUMBER: 09/767,597
11 <141> CURRENT FILING DATE: 2001-01-22
13 <150> PRIOR APPLICATION NUMBER: 09/548,933
14 <151> PRIOR FILING DATE: 2000-04-13
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 774
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
27        cation channel 3 (HAC3)
29 <400> SEQUENCE: 1
30 Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
31  1               5                   10                  15
33 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
34              20                  25                  30
36 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
37          35                  40                  45
39 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
40      50                  55                  60
42 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
43  65                  70                  75                  80
45 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
46              85                  90                  95
48 Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
49              100                 105                 110
51 Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
52          115                 120                 125
54 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
55      130                 135                 140
57 Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
58 145                 150                 155                 160
60 Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
61              165                 170                 175
63 Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
64              180                 185                 190
66 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
67              195                 200                 205
69 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
70      210                 215                 220
72 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
```

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73 225                   230                 235                  240
75 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
76               245                 250                 255
78 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
79           260                 265                 270
81 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
82           275                 280                 285
84 Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys
85       290                 295                 300
87 Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val
88 305                 310                 315                 320
90 Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala
91               325                 330                 335
93 Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser
94           340                 345                 350
96 Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu
97           355                 360                 365
99 Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile
100       370                 375                 380
102 His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu
103 385                 390                 395                 400
105 Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn
106               405                 410                 415
108 Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala
109           420                 425                 430
111 Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val
112           435                 440                 445
114 Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
115       450                 455                 460
117 Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala
118 465                 470                 475                 480
120 Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu
121               485                 490                 495
123 Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys
124 ·             500                 505                 510
126 Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu
127           515                 520                 525
129 Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu
130       530                 535                 540
132 Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu
133 545                 550                 555                 560
135 Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln
136               565                 570                 575
138 His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr
139           580                 585                 590
141 Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His
142           595                 600                 605
144 Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu
145       610                 615                 620
```

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```
147 Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
148 625             630             635             640
150 Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
151             645             650             655
153 Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
154             660             665             670
156 Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
157         675             680             685
159 Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Gly Arg Arg
160     690             695             700
162 Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
163 705             710             715             720
165 Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
166             725             730             735
168 Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
169             740             745             750
171 Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
172         755             760             765
174 Gln Leu Ser Ala Asn Met
175     770
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 2325
180 <212> TYPE: DNA
181 <213> ORGANISM: Homo sapiens
183 <220> FEATURE:
184 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
185       cation channel 3 (HAC3)
187 <400> SEQUENCE: 2
188 atggaggcag agcagcggcc ggcggcgggg gccagcgaag gggcgacccc tggactggag 60
189 gcggtgcctc ccgttgctcc cccgcctgcg accgcggcct caggtccgat ccccaaatct 120
190 gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggt caacaagttc 180
191 tcccttcggg tgttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
192 gcggggggcct ggatcatcca cccctacagc gacttccggt tttactggga cctgatcatg 300
193 ctgctgctga tggtgggggaa cctcatcgtc ctgcctgtgg gcatcacctt cttcaaggag 360
194 gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
195 ctggtgctca acttccgaac gggcatcgtg gtggaggagg gtgctgagat cctgctggca 480
196 ccgcgggcca tccgcacgcg ctacctgcgc acatggttcc tggttgacct catctcttct 540
197 atccctgtgg attacatctt cctagtggtg gagctggagc acggttgga cgctgaggtc 600
198 tacaaaacgg cacgggccct acgcatcgtt cgcttcacca agatcctaag cctgctgagg 660
199 ctgctccgcc tctcccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
200 acctatgacc tggccagtgc tgtggttcgc atcttcaacc tcattgggat gatgctgctg 780
201 ctatgtcact gggatggctg tctgcagttc ctggtgccca tgctgcagga cttccctccc 840
202 gactgctggg tctccatcaa ccacatggtg aaccactcgt ggggccgcca gtattcccat 900
203 gccctgttca aggccatgag ccacatgctg tgcattggct atgggcagca ggcacctgta 960
204 ggcatgcccg acgtctggct caccatgctc agcatgatcg taggtgccac atgctacgcc 1020
205 atgttcatcg gccatgccac ggcactcatc cagtccctgg actcttcccg gcgtcagtac 1080
206 caggagaagt acaagcaggt ggagcagtac atgtccttcc acaagctgcc agcagacacg 1140
207 cggcagcgca tccacgagta ctatgagcac cgctaccagg gcaagatgtt cgatgaggaa 1200
208 agcatcctgg gcgagctgag cgagccgctt cgcgaggaga tcattaactt cacctgtcgg 1260
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Output Set: N:\CRF3\12192001\I767597.raw

```
209 ggcctggtgg cccacatgcc gctgtttgcc catgccgacc ccagcttcgt cactgcagtt 1320
210 ctcaccaagc tgcgctttga ggtcttccag ccgggggatc tcgtggtgcg tgagggctcc 1380
211 gtggggagga agatgtactt catccagcat gggctgctca gtgtgctggc ccgcggcgcc 1440
212 cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgct aactaggggc 1500
213 cggcgcacag ccagtgttcg ggctgacacc tactgccgcc tttactcact cagcgtggac 1560
214 catttcaatg ctgtgcttga ggagttcccc atgatgcgcc gggcctttga gactgtggcc 1620
215 atggatcggc tgctccgcat cggcaagaag aattccatac tgcagcggaa gcgctccgag 1680
216 ccaagtccag gcagcagtgg tggcatcatg gagcagcact tggtgcaaca tgacagagac 1740
217 atggctcggg gtgttcgggg tcgggccccg agcacaggag ctcagcttag tggaaagcca 1800
218 gtactgtggg agccactggt acatgcgccc cttcaggcag ctgctgtgac ctccaatgtg 1860
219 gccattgccc tgactcatca gcggggccct ctgccctct ccctgactc tccagccacc 1920
220 ctccttgctc gctctgcttg gcgctcagca ggctctccag cttccccgct ggtgcccgtc 1980
221 cgagctggcc catgggcatc cacctcccgc ctgcccgccc cacctgcccg aaccctgcac 2040
222 gccagcctat cccgggcagg gcgctcccag gtctccctgc tgggtccccc tccaggagga 2100
223 ggtggacggc ggctaggacc tcggggccgc ccactctcag cctcccaacc ctctctgcct 2160
224 cagcgggcaa caggcgatgg ctctcctggg cgtaagggat caggaagtga gcggctgcct 2220
225 ccctcagggc tcctggccaa acctccaagg acagcccagc cccccaggcc accagtgcct 2280
226 gagccagcca caccccgggg tctccagctt tctgccaaca tgtaa                  2325
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 24
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
236       primer
238 <400> SEQUENCE: 3
239 cagccatgga ggcagagcag cggc                                       24
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 28
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
249       primer
251 <400> SEQUENCE: 4
252 ggaggagatc tttcacatga catacgac                                   28
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 24
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
262       primer
264 <400> SEQUENCE: 5
265 agtaggatcc atcggtgagg cgtg                                       24
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 27
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 12/19/2001
PATENT APPLICATION: US/09/767,597   TIME: 13:23:59

           Input Set : N:\Crf3\RULE60\09767597.txt
           Output Set: N:\CRF3\12192001\I767597.raw

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273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
275      primer
277 <400> SEQUENCE: 6
278 ttacatgttg gcagaaagct ggagacc                                      27
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 29
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
288      amplification primer
290 <220> FEATURE:
291 <221> NAME/KEY: modified_base
292 <222> LOCATION: (24)
293 <223> OTHER INFORMATION: n = g, a, c or t
295 <400> SEQUENCE: 7
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W--> 296 tgggaggaga tcttycayat gacntayga   29
```
299 <210> SEQ ID NO: 8
300 <211> LENGTH: 27
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
306      amplification primer
308 <220> FEATURE:
309 <221> NAME/KEY: modified_base
310 <222> LOCATION: (16)
311 <223> OTHER INFORMATION: n = g, a, c or t
313 <220> FEATURE:
314 <221> NAME/KEY: modified_base
315 <222> LOCATION: (25)
316 <223> OTHER INFORMATION: n = g, a, c or t
318 <400> SEQUENCE: 8
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W--> 319 cgtctcgaat gcccknckca tcatngg   27
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322 <210> SEQ ID NO: 9
323 <211> LENGTH: 26
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence:first round 5'
329      RACE gene specific primer
331 <400> SEQUENCE: 9
332 cctgctgccc atagccaatg cacagc                                       26
335 <210> SEQ ID NO: 10
336 <211> LENGTH: 25
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 12/19/2001
PATENT APPLICATION: **US/09/767,597**   TIME: 13:24:00

Input Set : **N:\Crf3\RULE60\09767597.txt**
Output Set: **N:\CRF3\12192001\I767597.raw**

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8